

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 04:23:52 ; Search time 1619.26 Seconds

(without alignments)
9956.972 Million cell updates/sec

Title: US-09-856-766-1

Perfect score: 554
Sequence: 1 cctctatgcctcctcaggtc.....aagggcgtgagaccaca 554

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

T number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

09856766
Attach Paper M13

Database: GenBank:
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_or:*
21: em_ov:*
22: em_pac:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_un:*
28: em_vl:*
29: em_hgt:*
30: em_hgt_hum:*
31: em_hgt_inv:*
32: em_hgt_other:*
33: em_hgt_mus:*
34: em_hgt_pln:*
35: em_hgt_rtd:*
36: em_hgt_mam:*
37: em_hgt_vrt:*
38: em_sy:*
39: em_hgt_hum:*
40: em_hgt_mus:*
41: em_hgt_other:*

Pred. No. is the number of results predicted by chance to have a

Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554	100.0	9811	10 RNSOD2	X56600 Rat SOD-2 g
2	538.4	97.2	164373	2 AC108954	AC108954 Rattus no
3	325.4	58.7	203949	10 AL589878	AL589878 Mouse DNA
4	325.4	58.7	208568	2 AC127172	AC127172 Mus muscu
5	318.8	57.5	664	10 MUSMNSOD2	MUSMNSOD2 Mus muscu
6	214.2	38.7	2110	10 AF003694	AF003694 Mus muscu
7	194.8	35.2	336	10 S7883282	S7883282 Sod-2-manga
8	145.8	26.3	110000	2 AC074222_1	AC074222_1 Continuation (2 of
9	145.8	26.3	110000	2 AC074222_2	AC074222_2 Continuation (3 of
10	130.2	23.5	110000	2 AC074222_1	AC074222_1 Continuation (2 of
11	116	20.9	1438	10 RNMNSOD	RNMNSOD Rat mRNA fo
12	116	20.9	1438	6 AX401951	AX401951 Sequence
13	108.6	19.6	487	9 HUMMSDA	HUMMSDA Homo sapien
14	108.6	19.6	165802	9 AL135914	AL135914 Human DNA
15	108	19.5	836	10 BC018173	BC018173 Mus muscu
16	106.4	19.2	779	10 BC010548	BC010548 Mus muscu
17	106.4	19.2	897	10 MNMSODRX	MNMSODRX Mus muscu
18	105.8	19.1	12857	9 S77127	S77127 Homo sapien
19	105.8	19.1	969	6 AR054016	AR054016 DNA encodin
20	100.2	18.1	627	9 E08014	E08014 Sequence
21	100.2	18.1	969	6 AR146192	AR146192 Sequence
22	100.2	18.1	969	9 HSMNSODGE	HSMNSODGE Sequence
23	100.2	18.1	989	9 HSMNSUDIS	HSMNSUDIS Sequence
24	100.2	18.1	304	6 AX397183	AX397183 Human mRNA
25	100	18.1	522	6 A12179	A12179 H.sapiens m
26	100	18.1	535	6 A12178	A12178 H.sapiens m
27	100	18.1	600	6 A12180	A12180 Artificial
28	100	18.1	600	6 A12190	A12190 Artificial
29	100	18.1	600	6 A12191	A12191 Artificial
30	100	18.1	600	6 A12200	A12200 Nucleotide
31	100	18.1	603	6 E08013	E08013 H.sapiens m
32	100	18.1	627	6 AR06849	AR06849 DNA encodin
33	100	18.1	813	6 AR106627	AR106627 Sequence
34	100	18.1	813	6 AR106627	AR106627 Sequence
35	100	18.1	813	6 AR106627	AR106627 Sequence
36	100	18.1	813	6 AR106627	AR106627 Sequence
37	100	18.1	829	9 HSMNSODR	HSMNSODR Human mRNA
38	100	18.1	940	9 BC012423	BC012423 Homo sapi
39	100	18.1	1026	6 AX334340	AX334340 Sequence
40	100	18.1	1026	6 HSSOD	HSSOD Human mRNA
41	100	18.1	2555	9 AK097395	AK097395 Homo sapi
42	98.4	17.8	594	6 AR130379	AR130379 Sequence
43	98.4	17.8	609	6 E03557	E03557 Synthetic D
44	98.4	17.8	633	10 CP039843	CP039843 Cavia porce
45	98.4	17.8	681	6 AR130381	AR130381 Sequence

ALIGNMENTS

RESULT 1
RNSOD2
LOCUS RNSOD2 9811 bp DNA linear ROD 12-SEP-1996
DEFINITION Rat SOD-2 gene for manganese-containing superoxide dismutase.
ACCESSION X56600
VERSION X56600.1 GI:57272
KEYWORDS SOD2 gene; superoxide dismutase.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 9811)
AUTHORS Ho, Y. S.
TITLE Direct Submission

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OW nucleic - nucleic search, using sw model

Run on: June 9, 2003, 04:23:52 ; Search time 1362.05 Seconds

(without alignments)
9956.972 Million cell updates/sec

Title: US-09-856-766-2

Perfect score: 466

Sequence: 1 cgttagcgggttcgacagcagc.....ttacttgcgaatcagagcc 466

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

1 number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBank:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_srs:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: gb_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_srs:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rod:*

36: em_hcg_mam:*

37: em_hcg_vtc:*

38: em_sy:*

39: em_hgo_hum:*

40: em_hgo_mus:*

41: em_hgo_other:*

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ATTACH
PAPW NO 13

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	100.0	12857	S77127	S77127 Homo sapien
2	464.4	99.7	1984	9 HSM800535	AL050388 Homo sapi
3	464.4	99.7	165802	9 AL135914	AL135914 Human DNA
4	247	53.0	1617	9 BC016934	BC016934 Homo sapi
5	98.6	21.2	203949	10 AL589878	AL589878 Mouse DNA
6	98.6	21.2	208568	2 AC127172	AC127172 Mus muscu
7	98	21.0	2110	10 AF003694	AF003694 Mus muscu
8	97	20.8	684	10 MUSMNSD02	L35526 Mus musculu
9	93	20.0	164373	2 AC108954	AC108954 Rattus no
10	91	19.5	9811	10 RNSOD2	X56600 Rat SOD-2 g
11	72.2	15.5	110000	2 AC074222	Continuation (2 of
12	46.8	10.0	146383	2 AC116367	AC116367 Oryza sat
13	45.8	9.8	27263	2 AC106990	AC106990 Rattus no
14	44	9.4	150312	9 CNS01R1J	AL163813 Human chr
15	44	9.4	151171	2 AC020775	AC020775 Homo sapi
16	44	9.4	185636	2 AC027109	AC027109 Homo sapi
17	43.2	9.3	16258	6 AX348424	AX348424 Sequence
18	43.2	9.3	16258	6 AX348807	AX348807 Sequence
19	43	9.2	4904	9 AB037804	AB037804 Homo sapi
20	43	9.2	98078	9 AL451083	AL451083 Human DNA
21	43	9.2	157918	2 AL360019	AL360019 Homo sapi
22	43	9.2	158255	2 AC025695	AC025695 Homo sapi
23	42.8	9.2	172210	9 AC098656	AC098656 Homo sapi
24	42.6	9.1	17811	9 AC008634	AC008634 Homo sapi
25	42.6	9.1	135961	2 AC021288	AC021288 Homo sapi
26	42.6	9.1	149378	9 AC098708	AC098708 Homo sapi
27	42.4	9.1	167667	9 AC099329	AC099329 Homo sapi
28	42.4	9.1	180359	2 AC022064	AC022064 Homo sapi
29	42.2	9.1	28326	3 AC024808	AC024808 Caenorhab
30	42	9.0	17848	6 AX277865	AX277865 Sequence
31	42	9.0	17848	6 AX323550	AX323550 Sequence
32	42	9.0	17848	6 AX348363	AX348363 Sequence
33	41.8	8.9	167500	2 AC094710	AC094710 Rattus no
34	41.6	8.9	5678	6 AX346041	AX346041 Sequence
35	41.4	8.9	76976	8 AC006532	AC006532 Arabidops
36	41.4	8.9	158832	2 AC097950	AC097950 Rattus no
37	41.4	8.9	181719	2 AL592045	AL592045 Homo sapi
38	41.4	8.9	191233	2 AC122856	AC122856 Mus muscu
39	41.4	8.9	232180	2 AC021883	AC021883 Homo sapi
40	41.2	8.8	129320	9 HSDJ47M23	AL096816 Human DNA
41	41.2	8.8	148116	2 AC078838	AC078838 Homo sapi
42	41.2	8.8	159621	9 AC083801	AC083801 Homo sapi
43	41.2	8.8	174040	2 AC073950	AC073950 Homo sapi
44	41	8.8	105400	9 AC125492	AC125492 Homo sapi
45	41	8.8	106601	9 AL357352	AL357352 Human DNA

ALIGNMENTS

RESULT 1

S77127 12857 bp DNA linear PRI 05-JUN-2000

LOCUS Homo sapiens manganese superoxide dismutase gene, complete cds.

DEFINITION S77127

ACCESSION S77127.1 GI:998582

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 12857)

AUTHORS

Man,X.S., Devalaraja,M.N. and St Clair,D.K.

TITLE

Molecular structure and organization of the human manganese superoxide dismutase gene